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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: ELLIOTT et al.
Title: KINASES AND PHOSPHATASES
Appnl. No.: 10/554,917
Filing Date: 04/27/2007
Examiner: Unassigned
Art Unit: 1652
Conf. No.: 9780

TRANSMITTAL OF RESPONSE TO NOTICE TO COMPLY

Mail Stop SEQUENCE

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures, mailed February 26, 2009, in the above-identified application, transmitted herewith are the following documents:

Enclosed are:

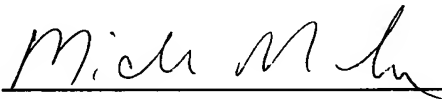
- [X] Return Copy of Notice to Comply including error pages (12 page).
- [X] Statement to Support Filing and Submission in accordance with 37 C.F.R. §§1.821-1.825 (1 page).
- [X] Sequence Listing (181 pages).
- [X] Computer Readable Format (1 Compact disk).
- [X] Amendment in Response to Notice Under 37 CFR §§ 1.821-825 (4 pages).

The Commissioner is hereby authorized to charge any fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by the credit card payment form being unsigned, providing incorrect information resulting in a rejected credit card transaction, or even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741.

Please direct all correspondence to the undersigned attorney or agent at the address indicated below.

Respectfully submitted,

Date: March 24, 2009

By _____

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Customer Number: 22428
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Michele M. Simkin
Attorney for Applicant
Registration No. 34,717



Notice to Comply

Application No.
10554917

Applicant(s)
ELLIOTT ET AL.

Examiner
SHERIDAN SWOPE

Art Unit
1652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-0731 or (571) 272-0951
For CRF Submission Help, call (571) 272-2510
PatentIn Software Program Support
Technical Assistance. 1-866-217-9197 or 703-305-3028 or 571-272-6845
PatentIn Software is Available At www.USPTO.gov

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

/SHERIDAN SWOPE/
Primary Examiner, Art Unit 1652



=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=15; hr=12; min=18; sec=18; ms=279;]

=====

Reviewer Comments:

<400> 3

Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile

1 5 10 15

Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln

20 25 30

Please remove the blank line between the amino acids and their respective numbers above. This error appears in subsequent amino acid sequences. Also, please remove the blank lines between rows of nucleotides (this appears in subsequent sequences).

(end of Sequence 86)

ttttatttta tttatTTTTT gatggagtct tgcactccag cctggtgaca gact 1914

PF-1506 PCT

1/94

WASH_1695548.1

Please remove the above three lines of text, which appear at the end of the submitted file.

Application No: 10554917

Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
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Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (13)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (15)
E 355	Empty lines found between the amino acid numbering and the
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Input Set:

Output Set:

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Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
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E 355	Empty lines found between the amino acid numbering and the
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E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31) POS (915)
E 330	Invalid protein , found in SEQID(86) POS (1)Invalid Protein:PCT

Input Set:

Output Set:

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Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 112	Upper case found in data; Found at position(1914) SeqId(86)
W 112	Upper case found in data; Found at position(1915) SeqId(86)
W 112	Upper case found in data; Found at position(1916) SeqId(86)
W 112	Upper case found in data; Found at position(1917) SeqId(86)
E 259	Found undefined lettercode; POS (1919) SEQID(86)
E 259	Found undefined lettercode; POS (1920) SEQID(86)
E 259	Found undefined lettercode; POS (1921) SEQID(86)
E 259	Found undefined lettercode; POS (1922) SEQID(86)
E 259	Found undefined lettercode; POS (1923) SEQID(86)
E 259	Found undefined lettercode; POS (1924) SEQID(86)
E 259	Found undefined lettercode; POS (1925) SEQID(86)
E 259	Found undefined lettercode; POS (1926) SEQID(86)
E 259	Found undefined lettercode; POS (1927) SEQID(86)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 1927 SEQID(86)
E 253	The number of bases differs from <211> Input: 1914 Calculated:1927 SEQID (86)

<110> INCYTE CORPORATION; ELLIOTT, Vicki S.;
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WILSON, Amy D.; JIN, Pei

<120> KINASES AND PHOSPHATASES

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				20					25					30

Asp	Gly	Lys	Gly	Thr	Leu	Leu	Ile	Arg	Asn	Gly	Ser	Glu	Thr	Thr
				35					40					45
Trp	Leu	Ser	Leu	Cys	Thr	Ala	Met	Ser	Pro	Leu	Thr	Thr	Glu	Ile
				50					55					60
Trp	Ala	Leu	Arg	Arg	Gly	Asn	Ser	Ser	Ala	Ser	Trp	Ser	Arg	Ala
				65					70					75
Ala	Ser	Gly	Gly	Arg	Arg	Ser	Pro							
				80										

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<211> 292

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<213> Homo sapiens

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Arg	Phe	Val	Met	Glu	Glu	Gly	Arg	Lys	Ala	Arg	Gly	Thr	Gly	Glu
				20					25					30
Leu	Thr	Gln	Leu	Leu	Asn	Ser	Leu	Cys	Thr	Ala	Val	Lys	Ala	Ile
				35					40					45
Ser	Ser	Ala	Val	Arg	Lys	Ala	Gly	Ile	Ala	His	Leu	Tyr	Gly	Ile
				50					55					60
Ala	Gly	Ser	Thr	Asn	Val	Thr	Gly	Asp	Gln	Val	Lys	Lys	Leu	Asp
				65					70					75
Val	Leu	Ser	Asn	Asp	Leu	Val	Met	Asn	Met	Leu	Lys	Ser	Ser	Phe
				80					85					90
Ala	Thr	Cys	Val	Leu	Val	Ser	Glu	Glu	Asp	Lys	His	Ala	Ile	Ile
				95					100					105
Val	Glu	Pro	Glu	Lys	Arg	Gly	Lys	Tyr	Val	Val	Cys	Phe	Asp	Pro
				110					115					120
Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp	Cys	Leu	Val	Ser	Val	Gly	Thr
				125					130					135
Ile	Phe	Gly	Ile	Tyr	Arg	Lys	Lys	Ser	Thr	Asp	Glu	Pro	Ser	Glu
				140					145					150
Lys	Asp	Ala	Leu	Gln	Pro	Gly	Arg	Asn	Leu	Val	Ala	Ala	Gly	Tyr
				155					160					165
Ala	Leu	Tyr	Gly	Ser	Ala	Thr	Met	Leu	Val	Leu	Ala	Met	Asp	Cys
				170					175					180
Gly	Val	Asn	Cys	Phe	Met	Leu	Asp	Pro	Asp	Asn	Ser	Ala	Pro	Tyr
				185					190					195
Gly	Ala	Arg	Tyr	Val	Gly	Ser	Met	Val	Ala	Asp	Val	His	Arg	Thr
				200					205					210
Leu	Val	Tyr	Gly	Gly	Ile	Phe	Leu	Tyr	Pro	Ala	Asn	Lys	Lys	Ser
				215					220					225
Pro	Asn	Gly	Lys	Leu	Arg	Leu	Leu	Tyr	Glu	Cys	Asn	Pro	Met	Ala
				230					235					240
Tyr	Val	Met	Glu	Lys	Ala	Gly	Gly	Met	Ala	Thr	Thr	Gly	Lys	Glu
				245					250					255
Ala	Val	Leu	Asp	Val	Ile	Pro	Thr	Asp	Ile	His	Gln	Arg	Ala	Pro
				260					265					270
Val	Ile	Leu	Gly	Ser	Pro	Asp	Asp	Val	Leu	Glu	Phe	Leu	Lys	Val
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					20				25					30
Arg	Gly	Val	Cys	Met	Thr	Asn	Cys	Pro	Thr	Leu	Ile	Val	Met	Val
				35					40					45
Gly	Leu	Pro	Ala	Arg	Gly	Lys	Thr	Tyr	Ile	Ser	Lys	Lys	Leu	Thr
				50					55					60
Arg	Tyr	Leu	Asn	Trp	Ile	Gly	Val	Pro	Thr	Arg	Glu	Phe	Asn	Val
				65					70					75
Gly	Gln	Tyr	Arg	Arg	Asp	Val	Val	Lys	Thr	Tyr	Lys	Ser	Phe	Glu
				80					85					90
Phe	Phe	Leu	Pro	Asp	Asn	Glu	Glu	Gly	Leu	Lys	Ile	Arg	Lys	Gln
				95					100					105
Cys	Ala	Leu	Ala	Ala	Leu	Arg	Asp	Val	Arg	Arg	Phe	Leu	Ser	Glu
				110					115					120
Glu	Gly	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg
				125					130					135
Glu	Arg	Arg	Ala	Thr	Ile	Phe	Asn	Phe	Gly	Glu	Gln	Asn	Gly	Tyr
				140					145					150
Lys	Thr	Phe	Phe	Val	Glu	Ser	Ile	Cys	Val	Asp	Pro	Glu	Val	Ile
				155					160					165
Ala	Ala	Asn	Ile	Val	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp	Tyr	Val
				170					175					180
Asn	Arg	Asp	Ser	Asp	Glu	Ala	Thr	Glu	Asp	Phe	Met	Arg	Arg	Ile
				185					190					195
Glu	Cys	Tyr	Glu	Asn	Ser	Tyr	Glu	Ser	Leu	Asp	Glu	Asp	Leu	Asp
				200					205					210
Arg	Asp	Leu	Ser	Tyr	Ile	Lys	Ile	Met	Asp	Val	Gly	Gln	Ser	Tyr
				215					220					225
Val	Val	Asn	Arg	Val	Ala	Asp	His	Ile	Gln	Ser	Arg	Ile	Val	Tyr
				230					235					240
Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr	Leu	Cys
				245					250					255
Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Leu	Lys	Gly	Arg	Ile	Gly	Gly
				260					265					270
Asp	Pro	Gly	Leu	Ser	Pro	Arg	Gly	Arg	Glu	Phe	Ala	Lys	Ser	Leu
				275					280					285
Ala	Gln	Phe	Ile	Ser	Asp	Gln	Asn	Ile	Lys	Asp	Leu	Lys	Val	Trp
				290					295					300
Thr	Ser	Gln	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala	Leu	Gly
				305					310					315
Val	Pro	Tyr	Glu	Gln	Trp	Lys	Val	Leu	Asn	Glu	Ile	Asp	Ala	Ser

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Tyr Glu Asp Leu Val Gln Arg Leu Glu	Pro Val Ile Met Glu Leu	
335	340	345
Glu Arg Gln Glu Asn Val Leu Val Ile	Cys His Gln Ala Val Met	
350	355	360
Arg Cys Leu Leu Ala Tyr Phe Leu Asp	Lys Ala Ala Glu Gln Leu	
365	370	375
Pro Tyr Leu Lys Cys Pro Leu His Thr	Val Leu Lys Leu Thr Pro	
380	385	390
Val Ala Tyr Gly Cys Lys Val Glu Ser	Ile Phe Leu Asn Val Ala	
395	400	405
Ala Val Asn Thr His Arg Asp Arg Pro	Gln Asn Val Asp Ile Ser	
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Arg Pro Pro Glu Glu Ala Leu Val Thr	Val Pro Ala His Gln	
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Arg Val Leu Ser Gly Asp Leu Gly Gln Leu Pro Thr Gly Ile Arg		
35	40	45
Asp Phe Val Glu His Ser Ala Arg Leu Cys Gln Pro Glu Gly Ile		
50	55	60
His Ile Cys Asp Gly Thr Glu Ala Glu Asn Thr Ala Thr Leu Thr		
65	70	75
Leu Leu Glu Gln Gln Gly Leu Ile Arg Lys Leu Pro Lys Tyr Asn		
80	85	90
Asn Cys Trp Leu Ala Arg Thr Asp Pro Lys Asp Val Ala Arg Val		
95	100	105
Glu Ser Lys Thr Val Ile Val Thr Pro Ser Gln Arg Asp Thr Val		
110	115	120
Pro Leu Pro Pro Gly Gly Ala Arg Gly Gln Leu Gly Asn Trp Met		
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Ser Pro Ala Asp Phe Gln Arg Ala Val Asp Glu Arg Phe Pro Gly		
140	145	150
Cys Met Gln Gly Arg Thr Met Tyr Val Leu Pro Phe Ser Met Gly		
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Pro Val Gly Ser Pro Leu Ser Arg Ile Gly Val Gln Leu Thr Asp		
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Ser Ala Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Leu Gly		
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Thr Pro Val Leu Gln Ala Leu Gly Asp Gly Asp Phe Val Lys Cys		
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Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg Tyr Leu Asn Trp
          35           40           45
Ile Gly Thr Pro Thr Lys Val Phe Asn Leu Gly Gln Tyr Arg Arg
          50           55           60
Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu Pro Asp Asn
          65           70           75
Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu
          80           85           90
Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly His Val Ala
          95          100          105
Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ser Leu Ile
          110          115          120
Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe Phe Ile Glu
          125          130          135
Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn Ile Arg Gln
          140          145          150
Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp Arg Glu Lys
          155          160          165
Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr Glu Val Asn
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His Ala Thr Trp

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          20           25           30

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Ser Leu Ile Leu	Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe	80	85	90
Phe Ile Glu Ser	Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn	95	100	105
Ile Arg Gln Val	Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp	110	115	120
Arg Glu Lys Val	Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr	125	130	135
Glu Val Asn Tyr	Gln Pro Leu Asp Glu Glu Leu Asp Ser His Leu	140	145	150
Ser Tyr Ile Lys	Ile Phe Asp Val Gly Thr Arg Tyr Met Val Asn	155	160	165
Arg Val Gln Asp	His Ile Gln Ser Arg Thr Val Tyr Tyr Leu Met	170	175	180
Asn Ile His Val	Thr Pro Arg Ser Ile Tyr Leu Cys Arg His Gly	185	190	195
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Ile Gln Ser Gln	Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His	230	235	240
Met Lys Arg Thr	Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr	245	250	255
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Glu Met Thr Tyr	Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe	275	280	285
Ala Leu Arg Asp	Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly	290	295	300
Glu Ser Tyr Glu	Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met	305	310	315
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Glu Leu Pro Tyr	Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu	350	355	360
Thr Pro Val Ala	Tyr Gly Cys Lys Val Glu Ser Ile Tyr Leu Asn	365	370	375
Val Glu Thr Val	Asn Thr His Arg Glu Lys Pro Glu Asn Val Asp	380	385	390
Ile Thr Arg Glu	Pro Glu Glu Ala Leu Asp Thr Val Pro Ala His	395	400	405
Tyr				

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<211> 426

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

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<400> 7

Met	Glu	Glu	Lys	Thr	Ser	Arg	Ile	Lys	Ala	Ser	Ile	Pro	Gln	Phe
1				5					10					15
Thr	Asn	Ser	Pro	Thr	Met	Val	Ile	Met	Val	Gly	Leu	Pro	Ala	Arg
				20					25					30
Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
				35					40					45
Ile	Gly	Thr	Pro	Thr	Lys	Asp	Asn	Met	Glu	Ala	Leu	Gln	Ile	Arg
				50					55					60
Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu	Lys	Asp	Val	His	Asn	Tyr	Leu
				65					70					75
Ser	His	Glu	Glu	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr
				80					85					90
Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile	Leu	Gln	Phe	Ala	Lys	Glu	His
				95					100					105
Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu	Ser	Ile	Cys	Asn	Asp	Pro	Gly
				110					115					120
Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp
				125					130					135
Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys	Val	Leu	Glu	Asp	Phe	Leu	Lys
				140					145					150
Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn	Tyr	Gln	Pro	Leu	Asp	Glu	Glu
				155					160					165
Leu	Asp	Ser	His	Leu	Ser	Tyr	Ile	Lys	Ile	Phe	Asp	Val	Gly	Thr
				170					175					180
Arg	Tyr	Met	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg	Thr
				185					190					195
Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr
				200					205					210
Leu	Cys	Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Ile	Arg	Gly	Arg	Ile
				215					220					225
Gly	Gly	Asp	Ser	Gly	Leu	Ser	Val	Arg	Gly	Lys	Gln	Tyr	Ala	Tyr
				230					235					240
Ala	Leu	Ala	Asn	Phe	Ile	Gln	Ser	Gln	Gly	Ile	Ser	Ser	Leu	Lys
				245					250					255
Val	Trp	Thr	Ser	His	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala
				260					265					270
Leu	Gly	Val	Pro	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp
				275					280					285
Ala	Gly	Val	Cys	Glu	Glu	Met	Thr	Tyr	Glu	Glu	Ile	Arg	Glu	His
				290					295					300
Tyr	Pro	Glu	Glu	Phe	Ala	Leu	Arg	Asp	Gln	Asp	Lys	Tyr	Arg	Tyr
				305					310					315
Arg	Tyr	Pro	Lys	Gly	Glu	Ser	Tyr	Glu	Asp	Leu	Val	Gln	Arg	Leu
				320					325					330
Glu	Pro	Val	Ile	Met	Glu	Leu	Glu							